Zurich-Basel Plant Science Center

PSC & Syngenta Symposium 2024

ETH zürich

PROGRAM

Opening session

Chair: Prof. Cyril Zipfel, PSC

Universität |

Zürich^{⊍z⊮}

10:00-10:10 Welcome Dr. Manuela Dahinden, PSC

10:10-10:30 Tracking and predicting resistance in Disease Control Dr. Gabriel Scalliet, Syngenta Senior Fellow

10:30-10:50 Microbiome management, soil health and sustainable agriculture Prof. Marcel van der Heijden, University of Zurich

10:50-11:10 Tackling soil-borne pathogens with beneficial compost microbes Dr. Pascale Flury, University of Basel

11:10-11:30 Questions & answers

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Chairs: Dr. Pascale Flury and Prof. Marcel van der Heijden, PSC

Universität

11:30-11:45

Improving biostimulants to cope with future climate for sustainable agriculture Dr. Marta Torres Bejar, University of Zurich

11:45-12:00

Toward the engineering of plant pattern recognition receptors for durable disease resistance Songyuan Zhang, University of Zurich, PhD student

12:00-13:45

Lunch break and tour through research facilities

13:45-14:00

Plant ecological airborne indicators for response, Plant Eco-AIR Dr. Meredith C. Schuman, Assistant Professor of Spatial Genetics, University of Zurich

14:00-14:15

Unearthing the mechanisms of carbon retention in soil and linking them to farmer practices

Dr. Luiz Alberto Domeignoz Horta, Previous postdoc at University of Zurich / Tenure-track INRAE Campus AgroParisTech Paris-Saclay University

14:15-14:30

Mycorrhiza-facilitated bioirrigation in intercropping systems in dryland agriculture as a new tool to stabilize and increase yields of small holder farmers Santiago Perez, University of Basel, PhD student

WEDNESDAY, March 27th, 2024



sture: by Pascale Flury, University of Base

14:30-14:45

Deciphering plant exudate and root microbiota dynamics during pathogen attack Charlotte Joller, University of Basel, PhD student

14:45-15:00 araChromID: Unraveling the Plant Epiproteome Miguel Wente, University of Zurich, PhD student

15:00-15:30 Coffee break

Closing session

Chair: Willy Rueegg, Syngenta, Head CPRB

15:30-16:00

Process-based soil-plant nitrogen cycle modelling to manage ecological systems Dr. Mafalda Nina, Syngenta Fellow

16:00-16:30 feminno spin off tbc

16:30-16:50 Questions & answers

16:50-17:00 Final remarks ^{Willy Rueegg}





Improving biostimulants to cope with future climate for

sustainable agriculture Leo Eberl (University of Zurich), Klaus Schlaeppi (University of Basel) and Monika Maurhofer (ETH Zurich)

Dr. Marta Torres Bejar, Postdoc Climate change with rapid acceleration of temperature increase and both water and soil salinization are the foremost challenges the agriculture sector is facing today. The major impact of changing environmental factors is the reduction of crop yield and quality. In this context, the aim of this project is to study how to make biostimulants (plant growth promoting rhizobacteria, PGPR) fit for the future.

We will study the impact of two major climate-induced stresses (temperature and salinity) in biostimulants to assess how to make these still beneficial at elevated temperatures or enhanced salinity. As a plant model we will use maize, the second most produced crop in the world. Despite the abundant data available on PGPR, the extent to which abiotic stresses may affect plant colonization abilities of these beneficial microorganisms is yet unknown and should be addressed before a breakthrough of this approach can be expected. Our aim in this project is to disentangle how the genetic traits involved in maize colonization of four beneficial model bacteria can change in different climatic scienarios. The genes and pathways identified in this study will be ideal targets to improve plant colonization of biostimulants under climate change-induced stresses. A better knowledge of such fitness genes would allow to engineer an improved and fitter version of the biostimulants we know nowadays.



Toward the engineering of plant pattern recognition receptors for durable disease resistance Cyril Zipfel (University of Zurich), Julia Vorholt (ETH Zurich) and Julia

Santiago (University of Lausanne) Songyuan Zhang, PhD student

Losses imposed by plant pathogens/pests are still a major burden on the yield and quality of crops – an issue only aggravated by climate change and tighter regulations on pesticides. Plant pattern recogni-tion receptors (PRRs) perceive conserved microbe-associated molecular patterns to induce immunity. While the interfamily transfer of PRRs has proven an effective strategy to improve plant disease resistance, identifying new PRRs from the natural repertoire is laborious and its

transfer involves transgenesis, which is still legally constrained in many countries. In addition, plant-associated microbes can evade PRR recognition in the constant co-evolution between plants and their microbiota, and thus deployment of novel or engineered efficient PRRs might be needed. In this project, we aim to develop a generally applicable methodology to engineer ligand-recognition specificity, which could be used ultimately for the precise genome enginee-ring of endogenous PRRs. As a proof-of-concept, we will engineer the flagellin receptor FLS2 as well as its co-receptor BAK1 to regain recognition of divergent flagellin-derived epitopes (flg22) from pathogens or commensals that evade recognition by plants. First, we will employ a rational design strategy based on the solved structure of the flg22-FLS2-BAK1 complex. A computational model will be developed to predict mutations on FLS2 and BAK1 that can confer recognition to evading flg22 variants. In parallel, a directed evolution strategy will be employed, which makes use of a yeast-based system coupling a synthetic FLS2-BAK1 complex formation with a high-throughput quantifiable output to screen/select for desired FLS2/BAK1 variants from a mutagenesis library. Identified gain-of-function mutations will be introduced into native FLS2 loci of diverse plant species, through CRISPR-based precise genome editing. The impact of engineered receptors will be evaluated through infection assays with both commensal and pathogenic bacteria. This project will not only provide a novel strategy for the precise molecular breeding of disease-resistant plants, but might also open doors for similar engineering of other plant receptors that can be used generally for crop improvement, not limited to disease resistance.



AMF-Mediated Interactions in Intercrops

Ansgar Kahmen (University of Basel) and Astrid Oberson (ETH Zurich) Santiago Perez Bernal, PhD student

Intercropping is a promising land-management practice for sustainable intensification. It involves the simultaneous cultivation of two or more crop species in the same field to boost plant yields. This is achieved by maximizing the productivity per unit area, as different crops utilize resources complementarily and enhance resource use efficiency. Arbuscular Mycorrhiza Fungi (AMF) is an important asset for sustainable agriculture as it forms symbiotic relationships with most

terrestrial plants. The benefits of this symbolic relationship will established, and numerous studies have demonstrated the positive impacts of AMF on plant yield, plant nutrition and improved resistance to both environmental and biotic stressors. Our focus came to investigate the AMF-mediated benefits in intercrops. We examined the mycorrhizal depen-dencies, (the extent to which various crops depend on AMF for optimal growth) to determine if overyielding (higher productivity in intercrops) is due to increased reliance on AMF as opposed to monoculture systems. We also investigated the impact of AMF enhancing resource availability via rhizobacteria-mediated synergies, which we anticipated would aid legumes in competing with non-fixing plants by raising the percentage of N they take up from the atmosphere. Lastly, we investigated if mineral fertilizers may modify the complementing effects mediated by AMF.



araChromID: Unraveling the Plant Epiproteome Sylvain Biscof (University of Zurich), Kirsten Bomblies (ETH Zurich) **Miguel Wente, PhD student** As the global climate continues to change, environmental stresses

such as extreme temperature and drought are becoming increasingly common and threaten to diminish the world's agricultural output. To cope with these challenges, the hardiness and stress resistance of our crops must be increased. In addition to genetic adaptation, plants have evolved epigenetic mechanisms to respond to biotic and abiotic stresses. Chromatin modifications and DNA methylation are important epigenetic components of gene regulation which affect how

rapidly and efficiently plants respond to environmental stresses. Despite all the research in the field, many proteins involved in depositing, removing, or interacting with these chromatin mo-difications and DNA methylation are still unknown. In the Bischof lab we have established a new method in plants that allows for the identification of proteins that "read", "write" or "erase" histone post-translational modifications. This method, known as araChromID, is unique in that it is executed in vivo and therefore could offer a more reliable prediction of the native state of the plants epiproteomic landscape.

With araChromID, I recently uncovered a group of four plant proteins (EML1,2,3,4) which appe ar to play a pivotal role in how rapidly and efficiently plants respond to environmental stresses. Research into the EML family proteins remains limited, but existing studies implicate a potential role in chromatin regulation, seed development and stress response, suggesting an involve-ment in plant defense mechanisms against environmental challenges. My goal is to unravel their specific molecular function and unveil novel targets for improving plant resilience to environmental stresses, thereby enhancing agricultural sustainability and yield.



Unearthing the mechanisms of carbon retention in soil and linking them to farmer practices

Anna-Liisa Laine (University of Zurich) and Ansgar Kahmen (University of Basel

Dr. Luiz Alberto Domeignoz Horta, Postdoc Soils are the largest and most dynamic terrestrial carbon (C) pool, storing 2000 Pg of C more than the atmosphere and biosphere combi-ned. However, agriculture has caused the loss of approximately 60 Pg soil C since the beginning of industrial period. Despite this, improving agricultural practices can also be used to counteract rising CO₂ levels.

As agroecosystems represent over 40% of earth surface today, they must be part of the solutions put in action to mitigate climate change. The utility of "carbon farming" – or the use of management practices to maximize soil carbon storage – is currently limited by a poor understanding of how the plants which input carbon to soil and the microbes which determine its fate there interact with one-another. Here we will elucidate the potential of different plant functional types to foster soil organic matter formation and persistence in soils though their interactions with soil microbial communities. By characterizing the molecular signature of biomass from diverse plant functional types in lab and field experiments characterized by distinct plant communities, we will evaluate the hypothesis that more molecularly diverse soil organic matter (SOM) persists longer in soils. The distinct plant functional types are implemented within a long-term intercropping farming experiment which will allow us to bring our results into an agricultural context. This project will link various disciplines including plant functional ecology, microbiology, stable isotopes and soil biogeochemistry to shed light into how farmers can implement more sustainable practices and help sequester carbon back into soils.



Plant ecological airborne indicators for response, plant Eco-AIR Meredith C. Schuman (University of Zurich), Stefano Mintchev (ETH Zurich), Anke Buchholz (Syngenta)

Dr. Sergio Ramos, Postdoc

Global change, characterized by climate change and biodiversity loss, is aggravated by unsustainable monocropping practices. Mixed crop ping practices may not achieve the shorter-term yields per acre of intensive monocropping but can ensure more stable yields in the long term, and are amenable to sustainable intensification (SI). Mixed cropping and SI are more work- and knowledge-intensive for farmers due to more heterogeneous fields with different plants requiring different

management, and thus successful targeted management is critical, especially when yearly yield margins may be smaller. Precision agricultural tools, especially scalable approaches using drones for image capture, can support targeted management of heterogeneous fields. This is helpful in monocrops, where heterogeneity comes from environmental patchiness e.g., in water retention or pest load, indicating a need for diversified management; and it is even more important for mixed cropping. A current limitation is that imaging, even using hyperspectral sensors, is best at identifying plant stress responses in a later stage when using hyperspectral sensors, is best at identifying plant stress responses in a later stage when there is bulk damage to plant parts. Early-stage plant stress responses employ bioactive phy-tochemicals produced as a small percentage of biomass, which are challenging to assess in the "bulk measurement" from a drone-based image. Thus, while drone-based imaging supports adaptive management, it provides limited support for early interventions to prevent yield loss. However, some stress-responsive phytochemicals comprise a tailored "early warning system" evolved by plants; volatiles released to the environment for defence and communication. A promising SI practice, push-pull technology (PPT), even uses species-typical volatiles from intercrops and trap crops to defend a focal crop against pests, and thus plant volatiles should be very good indicators of SI effectiveness in this system. We will (1) develop a drone-based system to sample volatiles near individual plants, and of patches on the scale of PPT mixed cropping units, i.e., an intercropped patch or crop-trap crop interface; (2) identify volatile indicators from litera-ture and field measurements, and (3) demonstrate drone-based monitoring of volatile indicators for yield loss prevention in both monocrop and PPT mixed-crop maize fields.



Deciphering plant exudate and root microbiota dynamics during pathogen attack Klaus Schläppi (University of Basel) & Joëlle Schläpfer

(University of Zurich)

Charlotte Joller, PhD student

Plants under pathogen attack adjust the composition of their microbiome and thereby, enrich for beneficial strains with protective functions. However, it is currently unclear how plants modulate their microbial communities. Metabolites exported from roots are nutrients and signaling compounds to the microbial community. We hypothe-

size that altering the exudation of specific compounds presents the mechanistic link between microbe recognition and changes in the composition of plant-as-sociated microbial communities. The objective of this project is to understand how plants alter exudation under pathogen attack, resulting in a modulated root microbiome. To accomplish this, we employ a reductionistic approach by growing Arabidopsis thaliana in sterile microcosm systems, by simulating pathogen attack by the application of elicitors, and studying the effects on a synthetic bacterial community. We first establish an experimental setup permitting par-On a synthetic bacterial community, we first establish an experimental setup permitting par-alleled metabolic and microbial analyses, then we identify candidate metabolites changing in response to immune stimulation, validate their effects on microbes and finally, we reassess the relevance of these key exudate compounds under natural conditions. With this project, we will make a step towards understanding the mechanistic link between a plant host and its micro-biome during pathogen attack. The identification of such key exudate metabolites will permit there be adding towards authorized authorized pathogen attack and the permitfuture breeding towards cultivars with 'disease-protective microbiomes' as sustainable solution to control pathogen burden